

Priebe

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/790,043B

1632

DATE: 07/10/98
TIME: 14:41:41

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This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

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(1) General Information:

- (i) APPLICANT: Payne, David
Lonsdale, John
Milner, Peter
Pearson, Stewart
- (ii) TITLE OF INVENTION: FAB I
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Dechert Price & Rhoads
 - (B) STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: US
 - (F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows 95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/024,845
 - (B) FILING DATE: 28-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Falk, Stephen T
 - (B) REGISTRATION NUMBER: 36,795
 - (C) REFERENCE/DOCKET NUMBER: GM50005
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 215-994-2488

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/790,043BDATE: 07/10/98
TIME: 14:41:42

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47 (B) TELEFAX: 215-994-2222
48 (C) TELEX:
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51 (2) INFORMATION FOR SEQ ID NO:1:
52

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 771 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: double
57 (D) TOPOLOGY: linear
58
59

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61

62	ATGTTAAATC	TTGAAAACAA	AACATATGTC	ATCATGGGAA	TCGCTAATAA	GCGTAGTATT	60
63	GCTTTTGGTG	TCGCTAAAGT	TTTAGATCAA	TTAGGTGCTA	AATTAGTATT	TACTTACCGT	120
64	AAAGAACGTA	GCCGTAAAGA	GCTTGAAAAA	TTATTAGAAC	AATTAAATCA	ACCAGAAGCG	180
65	CACTTATATC	AAATTGATGT	TCAAAGCGAT	GAAGAGGTTA	TTAATGGTTT	TGAGCAAATT	240
66	GGTAAAGATG	TTGGCAATAT	TGATGGTGTA	TATCAATCAA	TCGCATTTCG	TAATATGGAA	300
67	GACTTACGCG	GACGCTTTTC	TGAAACTTCA	CGTGAAGGCT	TCTTGTTAGC	TCAAGACATT	360
68	AGTTCTTACT	CATTAACAAT	TGTGGCTCAT	GAAGCTAAAA	AATTAATGCC	AGAAGGTGGT	420
69	AGCATTGTTG	CAACAACATA	TTTAGGTGGC	GAATTCGCAG	TTCAAAATTA	TAATGTGATG	480
70	GGTGTGCTA	AAGCGAGCTT	AGAAGCAAAT	GTAAATATT	TAGCATTAGA	CTTAGGTCCT	540
71	GATAATATTC	GCGTTAATGC	AATTTTCAGCT	GGTCCAATCC	GTACATTAAG	TGCAAAAGGT	600
72	GTGGGTGGTT	TCAATACAAT	TCTTAAAGAA	ATCGAAGAGC	GTGCACCTTT	AAAACGTAAC	660
73	GTTGATCAAG	TAGAAGTAGG	TAAAACAGCG	GCTTACTTTR	TAAGTGACTT	ATCAAGTGGC	720
74	GTTACAGGTG	AAAATATTCA	TGTAGATAGC	GGATTCCACG	CAATTAAATA	A	771

75
76 (2) INFORMATION FOR SEQ ID NO:2:
77

78 (i) SEQUENCE CHARACTERISTICS:

79 (A) LENGTH: 256 amino acids
80 (B) TYPE: amino acid
81 (C) STRANDEDNESS: single
82 (D) TOPOLOGY: linear
83
84

85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
86

87	Met	Leu	Asn	Leu	Glu	Asn	Lys	Thr	Tyr	Val	Ile	Met	Gly	Ile	Ala	Asn
88	1				5					10					15	
89	Lys	Arg	Ser	Ile	Ala	Phe	Gly	Val	Ala	Lys	Val	Leu	Asp	Gln	Leu	Gly
90				20					25					30		
91	Ala	Lys	Leu	Val	Phe	Thr	Tyr	Arg	Lys	Glu	Arg	Ser	Arg	Lys	Glu	Leu
92			35					40				45				
93	Glu	Lys	Leu	Leu	Glu	Gln	Leu	Asn	Gln	Pro	Glu	Ala	His	Leu	Tyr	Gln
94		50					55				60					
95	Ile	Asp	Val	Gln	Ser	Asp	Glu	Glu	Val	Ile	Asn	Gly	Phe	Glu	Gln	Ile
96	65					70				75				80		
97	Gly	Lys	Asp	Val	Gly	Asn	Ile	Asp	Gly	Val	Tyr	His	Ser	Ile	Ala	Phe
98				85					90					95		
99	Ala	Asn	Met	Glu	Asp	Leu	Arg	Gly	Arg	Phe	Ser	Glu	Thr	Ser	Arg	Glu

100				100				105					110			
101	Gly	Phe	Leu	Leu	Ala	Gln	Asp	Ile	Ser	Ser	Tyr	Ser	Leu	Thr	Ile	Val
102			115					120					125			
103	Ala	His	Glu	Ala	Lys	Lys	Leu	Met	Pro	Glu	Gly	Gly	Ser	Ile	Val	Ala
104		130					135					140				
105	Thr	Thr	Tyr	Leu	Gly	Gly	Glu	Phe	Ala	Val	Gln	Asn	Tyr	Asn	Val	Met
106	145				150						155					160
107	Gly	Val	Ala	Lys	Ala	Ser	Leu	Glu	Ala	Asn	Val	Lys	Tyr	Leu	Ala	Leu
108				165						170					175	
109	Asp	Leu	Gly	Pro	Asp	Asn	Ile	Arg	Val	Asn	Ala	Ile	Ser	Ala	Gly	Pro
110			180					185						190		
111	Ile	Arg	Thr	Leu	Ser	Ala	Lys	Gly	Val	Gly	Gly	Phe	Asn	Thr	Ile	Leu
112		195						200					205			
113	Lys	Glu	Ile	Glu	Glu	Arg	Ala	Pro	Leu	Lys	Arg	Asn	Val	Asp	Gln	Val
114		210				215						220				
115	Glu	Val	Gly	Lys	Thr	Ala	Ala	Tyr	Leu	Leu	Ser	Asp	Leu	Ser	Ser	Gly
116	225				230						235					240
117	Val	Thr	Gly	Glu	Asn	Ile	His	Val	Asp	Ser	Gly	Phe	His	Ala	Ile	Lys
118				245						250					255	

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SEQUENCE VERIFICATION REPORT
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Original Text